

**RAW SEQUENCE LISTING
PATENT APPLICATION US/09/756,186**

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#0100
DATE: 03/22/2001
TIME: 23:09:14

INPUT SET: S36550.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

1 **SEQUENCE LISTING**
2

3 (1) General Information:

4
5 (i) APPLICANT: Campbell, Robert K.
6 Jameson, Bradford A.
7 Chappel, Scott C.8
9 (ii) TITLE OF INVENTION: HYBRID PROTEINS

10 (iii) NUMBER OF SEQUENCES: 22

11 (iv) CORRESPONDENCE ADDRESS:

12
13 (A) ADDRESSEE: BROWDY AND NEIMARK
14 (B) STREET: 419 Seventh Street N.W., Ste. 300
15 (C) CITY: Washington
16 (D) STATE: D.C.
17 (E) COUNTRY: USA
18 (F) ZIP: 22207

19 (v) COMPUTER READABLE FORM:

20
21 (A) MEDIUM TYPE: Floppy disk
22 (B) COMPUTER: IBM PC compatible
23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

25 (vi) CURRENT APPLICATION DATA:

26
27 (A) APPLICATION NUMBER: 09/756,186
28 (B) FILING DATE:
29 (C) CLASSIFICATION:

30 (vii) PRIOR APPLICATION DATA:

31
32 (A) APPLICATION NUMBER: 08/804,166
33 (B) FILING DATE:
34 (C) CLASSIFICATION:

35 (viii) ATTORNEY/AGENT INFORMATION:

36
37 (A) NAME: Browdy, Roger L.
38 (B) REGISTRATION NUMBER: 25,618
39 (C) REFERENCE/DOCKET NUMBER: CAMPBELL=2A

40 (ix) TELECOMMUNICATION INFORMATION:

41
42 (A) TELEPHONE: (202) 628-5197
43 (B) TELEFAX: (202) 737-352844
45 (2) INFORMATION FOR SEQ ID NO:1:**ENTERED**

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47			
48	(i) SEQUENCE CHARACTERISTICS:		
49	(A) LENGTH: 1049 base pairs		
50	(B) TYPE: nucleic acid		
51	(C) STRANDEDNESS: single		
52	(D) TOPOLOGY: linear		
53	(ii) MOLECULE TYPE: cDNA		
54			
55	(ix) FEATURE:		
56	(A) NAME/KEY: CDS		
57	(B) LOCATION: 278..1047		
58			
59	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:		
60			
61	TCCACATGGC TACAGGTAAG CGCCCCTAAA ATCCCTTGG GCACAATGTG TCCTGAGGGG	60	
62			
63	AGAGGCAGCG ACCTGTAGAT GGGACGGGGG CACTAACCCCT CAGGTTTGGG GCTTCTCAAT	120	
64			
65	CTCACTATCG CCATGTAAGC CCAGTATTG GCCAATCTCA GAAAGCTCCT CCTCCCTGGA	180	
66			
67	GGGATGGAGA GAGAAAAACA AACAGCTCCT GGAGCAGGGA GAGTGCTGGC CTCTTGCTCT	240	
68			
69	CCGGCTCCCT CTGTTGCCCT CTGGTTCTC CCCAGGC TCC CGG ACG TCC CTG CTC	295	
70	Ser Arg Thr Ser Leu Leu		
71	1	5	
72			
73	CTG GCT TTT GGC CTG CTC TGC CTG CCC TGG CTT CAA GAG GGC AGT GCC	343	
74	Leu Ala Phe Gly Leu Leu Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala		
75	10	15	20
76			
77	GAT AGT GTG TGT CCC CAA GGA AAA TAT ATC CAC CCT CAA AAT AAT TCC	391	
78	Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser		
79	25	30	35
80			
81	ATT TGC TGT ACC AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC TGT	439	
82	Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys		
83	40	45	50
84			
85	CCA GGC CCG GGG CAG GAT ACG GAC TGC AGG GAG TGT GAG AGC GGC TCC	487	
86	Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser		
87	55	60	65
88		70	
89	CCA GGC CCG GGG CAG GAT ACG GAC TGC AGG GAG TGT GAG AGC GGC TCC	535	
90	Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser		
91	75	80	85
92			
93	TTC ACC GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC AGC TGC TCC AAA	583	
94	Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys		
95	90	95	100
96			
97	TGC CGA AAG GAA ATG GGT CAG GTG GAG ATC TCT TCT TGC ACA GTG GAC	631	
98	Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp		
99	105	110	115

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100					
101	AGT GAA AAC CTT TTC CAG TGC TTC AAT TGC AGC CTC TGC CTC AAT GGG				679
102	Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly				
103	120	125	130		
104					
105	ACC GTG CAC CTC TCC TGC CAG GAG AAA CAG AAC ACC GTG TGC ACC TGC				727
106	Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys				
107	135	140	145	150	
108					
109	CAT GCA GGT TTC TTT CTA AGA GAA AAC GAG TGT GTC TCC TGT GCC GGT				775
110	His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ala GLY				
111	155	160	165		
112					
113	GCT GCC CCA GGT TGC CCA GAA TGC ACG CTA CAG GAA AAC CCA TTC TTC				823
114	Ala Ala Pro Gly Cys Pro Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe				
115	170	175	180		
116					
117	TCC CAG CCG GGT GCC CCA ATA CTT CAG TGC ATG GGC TGC TGC TTC TCT				871
118	Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys Met Gly Cys Cys Phe Ser				
119	185	190	195		
120					
121	AGA GCA TAT CCC ACT CCA CTA AGG TCC AAG AAG ACG ATG TTG GTC CAA				919
122	Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln				
123	200	205	210		
124					
125	AAG AAC GTC ACC TCA GAG TCC ACT TGC TGT GTA GCT AAA TCA TAT AAC				967
126	Lys Asn Val Thr Ser Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn				
127	215	220	225	230	
128					
129	AGG GTC ACA GTC ATG GGG GGT TTC AAA GTG GAG AAC CAC ACG GGG TGC				1015
130	Arg Val Thr Val Met Gly Gly Phe Lys Val Glu Asn His Thr Gly Cys				
131	235	240	245		
132					
133	CAC TGC AGT ACT TGT TAT TAT CAC AAA TCT TA AG				1049
134	His Cys Ser Thr Cys Tyr Tyr His Lys Ser				
135	250	255			
136					
137					
138					
139					
140	(2) INFORMATION FOR SEQ ID NO:2:				
141					
142	(i) SEQUENCE CHARACTERISTICS:				
143	(A) LENGTH: 256 amino acids				
144	(B) TYPE: amino acid				
145	(D) TOPOLOGY: linear				
146					
147	(ii) MOLECULE TYPE: protein				
148					
149	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:				
150					
151	Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu Cys Leu Pro Trp				
152	1	5	10	15	

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153
154 Leu Gln Glu Gly Ser Ala Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile
155 20 25 30
156
157 His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr
158 35 40 45
159
160 Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg
161 50 55 60
162
163 Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu Arg His
164 65 70 75 80
165
166 Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile
167 85 90 95
168
169 Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn
170 100 105 110
171
172 Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys
173 115 120 125
174
175 Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln
176 130 135 140
177
178 Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu
179 145 150 155 160
180
181 Cys Val Ser Cys Ala Gly Ala Ala Pro Gly Cys Pro Glu Cys Thr Leu
182 165 170 175
183
184 Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys
185 180 185 190
186
187 Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys
188 195 200 205
189
190 Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser Glu Ser Thr Cys Cys
191 210 215 220
192
193 Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met Gly Gly Phe Lys Val
194 225 230 235 240
195
196 Glu Asn His Thr Gly Cys His Cys Ser Thr Cys Tyr Tyr His Lys Ser
197 245 250 255
198
199
200 (2) INFORMATION FOR SEQ ID NO:3:
201
202 (i) SEQUENCE CHARACTERISTICS:
203 (A) LENGTH: 1202 base pairs
204 (B) TYPE: nucleic acid
205 (C) STRANDEDNESS: single

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206	(D) TOPOLOGY: linear	
207		
208	(ii) MOLECULE TYPE: cDNA	
209		
210	(ix) FEATURE:	
211	(A) NAME/KEY: CDS	
212	(B) LOCATION: 279..1199	
213		
214	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:	
215		
216	CTCGAGATGG CTACAGGTAA GCGCCCTAA AATCCCTTG GGCACAATGT GTCCTGAGGG	60
217		
218	GAGAGGTAGC GACCTGTAGA TGGGACGGGG GCACTAACCC TGAGGTTTGG GGCTTCTGAA	120
219		
220	TGTGAGTATC GCCATGTAAG CCCAGTATTG GGCCAATGTC AGAAAGCTCC TGGTCCCTGG	180
221		
222	AGGGATGGAG AGAGAAAAAC AAACAGCTCC TGGAGCAGGG AGAGTGCTGG CCTCTTGCTC	240
223		
224	TCCGGCTCCC TCTGTTGCC C TGTGGTTCTT CCCCAGGC TCC CGG ACG TCC CTG	293
225	Ser Arg Thr Ser Leu	
226		
227	260	
228	CTC CTG GCT TTT GGC CTG CTC TGC CTG CCC TGG CTT CAA GAG GGC AGT	341
229	Leu Leu Ala Phe Gly Leu Leu Cys Leu Pro Trp Leu Gln Glu Gly Ser	
230	265 270 275	
231		
232	GCC GAT AGT GTG TGT CCC CAA GGA AAA TAT ATC CAC CCT CAA AAT AAT	389
233	Ala Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn	
234	280 285 290	
235		
236	TCG ATT TGC TGT ACC AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC	437
237	Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp	
238	295 300 305	
239		
240	TGT CCA GGC CCG GGG CAG GAT ACG GAC TGC AGG GAG TGT GAG AGC GGC	485
241	Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly	
242	310 315 320 325	
243		
244	TCT TTC ACC GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC AGC TGC TCC	533
245	Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser	
246	330 335 340	
247		
248	AAA TGC CGA AAG GAA ATG GGT CAG GTG GAG ATC TCT TCT TGC ACA GTG	581
249	Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val	
250	345 350 355	
251		
252	GAC CGG GAC ACC GTG TGT GGC TGC AGG AAG AAC CAG TAC CGG CAT TAT	629
253	Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr	
254	360 365 370	
255		
256	TGG AGT GAA AAC CTT TTC CAG TGC TTC AAT TGC AGC CTC TGC CTC AAT	677
257	Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn	
258	375 380 385	

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SEQUENCE VERIFICATION REPORT
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